

SEQUENCE LISTING

<110> E.I. duPont de Nemours and Company, Inc.
Suh, Wonchul
Rouviere, Pierre

<120> PARALLEL CHROMOSOMAL STACKING OF TRAITS IN BACTERIA

<130> CL2026 US NA

<150> US 60/434773

<151> 2002-12-19

<160> 43

<170> PatentIn version 3.2

<210> 1

<211> 912

<212> DNA

<213> Pantoea stewartii

<220>

<221> misc_feature

<222> (1)..(3)

<223> Alternative start codon usage TTG instead of ATG

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tgcgcggttg aaatggtgca tgctgcctcg ctgattctgg atgatatgcc ctgcatggac	300
gatgcgcaga tgcgtcgggg gcgtccacc attcacacgc agtacggtga acatgtggcg	360
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gtcgaagaac gcctgcgaca gcatttgcg ctaggcagtg aacacctttc cgcgcatgc	840
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<212> PRT

<213> Pantoea stewartii

<400> 2

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20 25 30

Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr
35 40 45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Thr Ala
50 55 60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65 70 75 80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
85 90 95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
100 105 110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
115 120 125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
130 135 140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145 150 155 160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
165 170 175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
180 185 190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
195 200 205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
210 215 220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225 230 235 240

Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
245 250 255

Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
260 265 270

Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln
Page 2

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Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser
 290 295 300

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 <213> Pantoea stewartii

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 gct ctg caa aac ctt gct cag gaa tta gtg gcc cgc ggt cat cgt gtt 96
 Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
 20 25 30
 acg ttt ttt cag caa cat gac tgc aaa gcg ctg gta acg ggc agc gat 144
 Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
 35 40 45
 atc gga ttc cag acc gtc gga ctg caa acg cat cct ccc ggt tcc tta 192
 Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
 50 55 60
 tcg cac ctg ctg cac ctg gcc gcg cac cca ctc gga ccc tcg atg tta 240
 Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
 65 70 75 80
 cga ctg atc aat gaa atg gca cgt acc agc gat atg ctt tgc cgg gaa 288
 Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
 85 90 95
 ctg ccc gcc gct ttt cat gcg ttg cag ata gag ggc gtg atc gtt gat 336
 Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
 100 105 110
 caa atg gag ccg gca ggt gca gta gtc gca gaa gcg tca ggt ctg ccg 384
 Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
 115 120 125
 ttt gtt tcg gtg gcc tgc gcg ctg ccg ctc aac cgc gaa ccg ggt ttg 432
 Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
 130 135 140
 cct ctg gcg gtg atg cct ttc gag tac ggc acc agc gat gcg gct cgg 480
 Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr 155 Ser Asp Ala Ala Arg
 145 150 155 160
 gaa cgc tat acc acc agc gaa aaa att tat gac tgg ctg atg cga cgt 528
 Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
 165 170 175
 cac gat cgt gtg atc gcg cat cat gca tgc aga atg ggt tta gcc ccg 576
 His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
 180 185 190
 cgt gaa aaa ctg cat cat tgt ttt tct cca ctg gca caa atc agc cag 624
 Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
 195 200 205

ttg atc ccc gaa ctg gat ttt ccc cgc aaa gcg ctg cca gac tgc ttt	672
Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe	
210 215 220	
cat gcg gtt gga ccg tta cgg caa ccc cag ggg acg ccg ggg tca tca	720
His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser	
225 230 235 240	
act tct tat ttt ccg tcc ccg gac aaa ccc cgt att ttt gcc tcg ctg	768
Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu	
245 250 255	
ggc acc ctg cag gga cat cgt tat ggc ctg ttc agg acc atc gcc aaa	816
Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys	
260 265 270	
gcc tgc gaa gag gtg gat gcg cag tta ctg ttg gca cac tgt ggc ggc	864
Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly	
275 280 285	
ctc tca gcc acg cag gca ggt gaa ctg gcc cgg ggc ggg gac att cag	912
Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln	
290 295 300	
gtt gtg gat ttt gcc gat caa tcc gca gca ctt tca cag gca cag ttg	960
Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu	
305 310 315 320	
aca atc aca cat ggt ggg atg aat acg gta ctg gac gct att gct tcc	1008
Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser	
325 330 335	
cgc aca ccg cta ctg gcg ctg ccg ctg gca ttt gat caa cct ggc gtg	1056
Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val	
340 345 350	
gca tca cga att gtt tat cat ggc atc ggc aag cgt gcg tct cgg ttt	1104
Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe	
355 360 365	
act acc agc cat gcg ctg gcg cgg cag att cga tcg ctg ctg act aac	1152
Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn	
370 375 380	
acc gat tac ccg cag cgt atg aca aaa att cag gcc gca ttg cgt ctg	1200
Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu	
385 390 395 400	
gca ggc ggc aca cca gcc gcc gcc gat att gtt gaa cag gcg atg cgg	1248
Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg	
405 410 415	
acc tgt cag cca gta ctc agt ggg cag gat tat gca acc gca cta tga	1296
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420 425 430	

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 <212> PRT
 <213> Pantoea stewartii

<400> 4

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20 25 30

Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
35 40 45

Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
50 55 60

Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65 70 75 80

Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
85 90 95

Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
100 105 110

Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
115 120 125

Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
130 135 140

Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145 150 155 160

Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
165 170 175

His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
180 185 190

Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
195 200 205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
210 215 220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225 230 235 240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
245 250 255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
260 265 270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
275 280 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
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295

300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305 310 315 320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
325 330 335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
340 345 350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
355 360 365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
370 375 380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385 390 395 400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
405 410 415

Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
420 425 430

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ggc ctt atc gcg ctc cgg ctt cag caa cag cat ccg gat atg cgg atc 96
Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile
20 25 30

ttg ctt att gag gcg ggt cct gag gcg gga ggg aac cat acc tgg tcc 144
Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
35 40 45

ttt cac gaa gag gat tta acg ctg aat cag cat cgc tgg ata gcg ccg 192
Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
50 55 60

ctt gtg gtc cat cac tgg ccc gac tac cag gtt cgt ttc ccc caa cgc 240
Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65 70 75 80

cgt cgc cat gtg aac agt ggc tac tac tgc gtg acc tcc cgg cat ttc 288
Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
85 90 95

gcc Ala	ggg Gly	ata Ile	ctc Leu 100	cgg Arg	caa Gln	cag Gln	ttt Phe	gga Gly 105	caa Gln	cat His	tta Leu	tgg Trp	ctg Leu 110	cat His	acc Thr	336
gcg Ala	gtt Val	tca Ser 115	gcc Ala	gtt Val	cat His	gct Ala	gaa Glu 120	tcg Ser	gtc Val	cag Gln	tta Leu	gcg Ala 125	gat Asp	ggc Gly	cgg Arg	384
att Ile	att Ile 130	cat His	gcc Ala	agt Ser	aca Thr	gtg Val 135	atc Ile	gac Asp	gga Gly	cgg Arg	ggg Gly 140	tac Tyr	acg Thr	cct Pro	gat Asp	432
tct Ser 145	gca Ala	cta Leu	cgc Arg	gta Val	gga Gly 150	ttc Phe	cag Gln	gca Ala	ttt Phe	atc Ile 155	ggg Gly	cag Gln	gag Glu	tgg Trp	caa Gln 160	480
ctg Leu	agc Ser	gcg Ala	ccg Pro	cat His 165	ggg Gly	tta Leu	tcg Ser	tca Ser 170	ccg Pro	att Ile	atc Ile	atg Met	gat Asp	gcg Ala 175	acg Thr	528
gtc Val	gat Asp	cag Gln	caa Gln 180	aat Asn	ggc Gly	tac Tyr	cgc Arg	ttt Phe 185	gtt Val	tat Tyr	acc Thr	ctg Leu 190	ccg Pro	ctt Leu	tcc Ser	576
gca Ala	acc Thr	gca Ala 195	ctg Leu	ctg Leu	atc Ile	gaa Glu	gac Asp 200	aca Thr	cac His	tac Tyr	att Ile	gac Asp 205	aag Lys	gct Ala	aat Asn	624
ctt Leu	cag Gln 210	gcc Ala	gaa Glu	cgg Arg	gcg Ala	cgt Arg 215	cag Gln	aac Asn	att Ile	cgc Arg	gat Asp 220	tat Tyr	gct Ala	gcg Ala	cga Arg	672
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ccc Pro	att Ile	acg Thr	tta Leu	acg Thr 245	ggc Gly	gat Asp	aat Asn	cgt Arg	cag Gln 250	ttt Phe	tgg Trp	caa Gln	cag Gln	caa Gln 255	ccg Pro	768
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tac Tyr	tcc Ser	cta Leu 275	ccg Pro	ctc Leu	gcg Ala	gtg Val 280	gcg Ala	ctg Leu	gcc Ala	gat Asp	cgt Arg	ctc Leu 285	agc Ser	gcg Ala	ctg Leu	864
gat Asp	gtg Val 290	ttt Phe	acc Thr	tct Ser	tcc Ser	tct Ser 295	gtt Val	cac His	cag Gln	acg Thr	att Ile 300	gct Ala	cac His	ttt Phe	gcc Ala	912
cag Gln 305	caa Gln	cgt Arg	tgg Trp	cag Gln	caa Gln 310	cag Gln	ggg Gly	ttt Phe	ttc Phe	cgc Arg 315	atg Met	ctg Leu	aat Asn	cgc Arg	atg Met 320	960
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ttc Phe	tat Tyr	ggc Gly	tta Leu 340	ccc Pro	gag Glu	gat Asp	ttg Leu	att Ile 345	gcc Ala	cgc Arg	ttt Phe	tat Tyr	gcg Ala 350	gga Gly	aaa Lys	1056
ctc Leu	acc Thr	gtg Val 355	acc Thr	gat Asp	cgg Arg	cta Leu	cgc Arg 360	att Ile	ctg Leu	agc Ser	ggc Gly	aag Lys 365	ccg Pro	ccc Pro	gtt Val	1104

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 370 375 380

<210> 6
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 <212> PRT
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Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
 35 40 45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
 50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
 65 70 75 80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
 85 90 95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
 100 105 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
 115 120 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
 130 135 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
 145 150 155 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
 165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
 180 185 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
 195 200 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
 210 215 220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu

225 230 235 240
 Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
 245 250 255
 Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
 260 265 270
 Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
 275 280 285
 Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
 290 295 300
 Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
 305 310 315 320
 Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
 325 330 335
 Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
 340 345 350
 Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
 355 360 365
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 370 375 380

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<220>
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 gca att cgt tta cag gcc gca ggt att cct gtt ttg ctg ctt gag cag 96
 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30
 cgc gac aag ccg ggt ggc cgg gct tat gtt tat cag gag cag ggc ttt 144
 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
 35 40 45
 act ttt gat gca ggc cct acc gtt atc acc gat ccc agc gcg att gaa 192
 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60
 gaa ctg ttt gct ctg gcc ggt aaa cag ctt aag gat tac gtc gag ctg 240
 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
 65 70 75 80

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Leu	Pro	Val	Thr	Pro	Phe	Tyr	Arg	Leu	Cys	Trp	Glu	Ser	Gly	Lys	Val	
				85					90					95		
ttc	aat	tac	gat	aac	gac	cag	gcc	cag	tta	gaa	gcg	cag	ata	cag	cag	336
Phe	Asn	Tyr	Asp	Asn	Asp	Gln	Ala	Gln	Leu	Glu	Ala	Gln	Ile	Gln	Gln	
			100					105					110			
ttt	aat	ccg	cgc	gat	gtt	gcg	ggg	tat	cga	gcg	ttc	ctt	gac	tat	tcg	384
Phe	Asn	Pro	Arg	Asp	Val	Ala	Gly	Tyr	Arg	Ala	Phe	Leu	Asp	Tyr	Ser	
		115					120					125				
cgt	gcc	gta	ttc	aat	gag	ggc	tat	ctg	aag	ctc	ggc	act	gtg	cct	ttt	432
Arg	Ala	Val	Phe	Asn	Glu	Gly	Tyr	Leu	Lys	Leu	Gly	Thr	Val	Pro	Phe	
	130					135					140					
tta	tcg	ttc	aaa	gac	atg	ctt	cgg	gcc	gcg	ccc	cag	ttg	gca	aag	ctg	480
Leu	Ser	Phe	Lys	Asp	Met	Leu	Arg	Ala	Ala	Pro	Gln	Leu	Ala	Lys	Leu	
	145				150					155					160	
cag	gca	tgg	cgc	agc	gtt	tac	agt	aaa	gtt	gcc	ggc	tac	att	gag	gat	528
Gln	Ala	Trp	Arg	Ser	Val	Tyr	Ser	Lys	Val	Ala	Gly	Tyr	Ile	Glu	Asp	
				165					170					175		
gag	cat	ctt	cgg	cag	gcg	ttt	tct	ttt	cac	tcg	ctc	tta	gtg	ggg	ggg	576
Glu	His	Leu	Arg	Gln	Ala	Phe	Ser	Phe	His	Ser	Leu	Leu	Val	Gly	Gly	
			180					185					190			
aat	ccg	ttt	gca	acc	tcg	tcc	att	tat	acg	ctg	att	cac	gcg	tta	gaa	624
Asn	Pro	Phe	Ala	Thr	Ser	Ser	Ile	Tyr	Thr	Leu	Ile	His	Ala	Leu	Glu	
		195					200					205				
cgg	gaa	tgg	ggc	gtc	tgg	ttt	cca	cgc	ggg	gga	acc	ggg	gcg	ctg	gtc	672
Arg	Glu	Trp	Gly	Val	Trp	Phe	Pro	Arg	Gly	Gly	Thr	Gly	Ala	Leu	Val	
	210					215					220					
aat	ggc	atg	atc	aag	ctg	ttt	cag	gat	ctg	ggc	ggc	gaa	gtc	gtg	ctt	720
Asn	Gly	Met	Ile	Lys	Leu	Phe	Gln	Asp	Leu	Gly	Gly	Glu	Val	Val	Leu	
	225				230					235					240	
aac	gcc	cgg	gtc	agt	cat	atg	gaa	acc	gtt	ggg	gac	aag	att	cag	gcc	768
Asn	Ala	Arg	Val	Ser	His	Met	Glu	Thr	Val	Gly	Asp	Lys	Ile	Gln	Ala	
				245					250					255		
gtg	cag	ttg	gaa	gac	ggc	aga	cgg	ttt	gaa	acc	tgc	gcg	gtg	gcg	tcg	816
Val	Gln	Leu	Glu	Asp	Gly	Arg	Arg	Phe	Glu	Thr	Cys	Ala	Val	Ala	Ser	
			260					265					270			
aac	gct	gat	gtt	gta	cat	acc	tat	cgc	gat	ctg	ctg	tct	cag	cat	ccc	864
Asn	Ala	Asp	Val	Val	His	Thr	Tyr	Arg	Asp	Leu	Leu	Ser	Gln	His	Pro	
		275					280					285				
gca	gcc	gct	aag	cag	gcg	aaa	aaa	ctg	caa	tcc	aag	cgt	atg	agt	aac	912
Ala	Ala	Ala	Lys	Gln	Ala	Lys	Lys	Leu	Gln	Ser	Lys	Arg	Met	Ser	Asn	
	290					295					300					
tca	ctg	ttt	gta	ctc	tat	ttt	ggg	ctc	aac	cat	cat	cac	gat	caa	ctc	960
Ser	Leu	Phe	Val	Leu	Tyr	Phe	Gly	Leu	Asn	His	His	His	Asp	Gln	Leu	
	305				310					315					320	
gcc	cat	cat	acc	gtc	tgt	ttt	ggg	cca	cgc	tac	cgt	gaa	ctg	att	cac	1008
Ala	His	His	Thr	Val	Cys	Phe	Gly	Pro	Arg	Tyr	Arg	Glu	Leu	Ile	His	
				325				330						335		
gaa	att	ttt	aac	cat	gat	ggg	ctg	gct	gag	gat	ttt	tcg	ctt	tat	tta	1056
Glu	Ile	Phe	Asn	His	Asp	Gly	Leu	Ala	Glu	Asp	Phe	Ser	Leu	Tyr	Leu	
			340					345					350			

cac	gca	cct	tgt	gtc	acg	gat	ccg	tca	ctg	gca	ccg	gaa	ggg	tgc	ggc	1104
His	Ala	Pro	Cys	Val	Thr	Asp	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Cys	Gly	
		355					360					365				
agc	tat	tat	gtg	ctg	gcg	cct	ggt	cca	cac	tta	ggc	acg	gcg	aac	ctc	1152
Ser	Tyr	Tyr	Val	Leu	Ala	Pro	Val	Pro	His	Leu	Gly	Thr	Ala	Asn	Leu	
	370					375					380					
gac	tgg	gcg	gta	gaa	gga	ccc	cga	ctg	cgc	gat	cgt	att	ttt	gac	tac	1200
Asp	Trp	Ala	Val	Glu	Gly	Pro	Arg	Leu	Arg	Asp	Arg	Ile	Phe	Asp	Tyr	
	385				390					395					400	
ctt	gag	caa	cat	tac	atg	cct	ggc	ttg	cga	agc	cag	ttg	gtg	acg	cac	1248
Leu	Glu	Gln	His	Tyr	Met	Pro	Gly	Leu	Arg	Ser	Gln	Leu	Val	Thr	His	
				405					410					415		
cgt	atg	ttt	acg	ccg	ttc	gat	ttc	cgc	gac	gag	ctc	aat	gcc	tgg	caa	1296
Arg	Met	Phe	Thr	Pro	Phe	Asp	Phe	Arg	Asp	Glu	Leu	Asn	Ala	Trp	Gln	
			420					425					430			
ggt	tcg	gcc	ttc	tcg	ggt	gaa	cct	att	ctg	acc	cag	agc	gcc	tgg	ttc	1344
Gly	Ser	Ala	Phe	Ser	Val	Glu	Pro	Ile	Leu	Thr	Gln	Ser	Ala	Trp	Phe	
		435					440					445				
cga	cca	cat	aac	cgc	gat	aag	cac	att	gat	aat	ctt	tat	ctg	ggt	ggc	1392
Arg	Pro	His	Asn	Arg	Asp	Lys	His	Ile	Asp	Asn	Leu	Tyr	Leu	Val	Gly	
		450				455					460					
gca	ggc	acc	cat	cct	ggc	gcg	ggc	att	ccc	ggc	gta	atc	ggc	tcg	gcg	1440
Ala	Gly	Thr	His	Pro	Gly	Ala	Gly	Ile	Pro	Gly	Val	Ile	Gly	Ser	Ala	
	465				470					475					480	
aag	gcg	acg	gca	ggc	tta	atg	ctg	gag	gac	ctg	att	tga				1479
Lys	Ala	Thr	Ala	Gly	Leu	Met	Leu	Glu	Asp	Leu	Ile					
				485					490							

<210> 8
 <211> 492
 <212> PRT
 <213> Pantoea stewartii

<400> 8

Met	Lys	Pro	Thr	Thr	Val	Ile	Gly	Ala	Gly	Phe	Gly	Gly	Leu	Ala	Leu
1				5					10					15	

Ala	Ile	Arg	Leu	Gln	Ala	Ala	Gly	Ile	Pro	Val	Leu	Leu	Leu	Glu	Gln
			20					25					30		

Arg	Asp	Lys	Pro	Gly	Gly	Arg	Ala	Tyr	Val	Tyr	Gln	Glu	Gln	Gly	Phe
		35					40					45			

Thr	Phe	Asp	Ala	Gly	Pro	Thr	Val	Ile	Thr	Asp	Pro	Ser	Ala	Ile	Glu
	50					55					60				

Glu	Leu	Phe	Ala	Leu	Ala	Gly	Lys	Gln	Leu	Lys	Asp	Tyr	Val	Glu	Leu
65					70					75					80

Leu	Pro	Val	Thr	Pro	Phe	Tyr	Arg	Leu	Cys	Trp	Glu	Ser	Gly	Lys	Val
				85					90					95	

Phe	Asn	Tyr	Asp	Asn	Asp	Gln	Ala	Gln	Leu	Glu	Ala	Gln	Ile	Gln	Gln

100					105					110					
Phe	Asn	Pro	Arg	Asp	Val	Ala	Gly	Tyr	Arg	Ala	Phe	Leu	Asp	Tyr	Ser
		115					120					125			
Arg	Ala	Val	Phe	Asn	Glu	Gly	Tyr	Leu	Lys	Leu	Gly	Thr	Val	Pro	Phe
	130					135					140				
Leu	Ser	Phe	Lys	Asp	Met	Leu	Arg	Ala	Ala	Pro	Gln	Leu	Ala	Lys	Leu
145					150					155					160
Gln	Ala	Trp	Arg	Ser	Val	Tyr	Ser	Lys	Val	Ala	Gly	Tyr	Ile	Glu	Asp
				165					170					175	
Glu	His	Leu	Arg	Gln	Ala	Phe	Ser	Phe	His	Ser	Leu	Leu	Val	Gly	Gly
			180					185					190		
Asn	Pro	Phe	Ala	Thr	Ser	Ser	Ile	Tyr	Thr	Leu	Ile	His	Ala	Leu	Glu
		195					200					205			
Arg	Glu	Trp	Gly	Val	Trp	Phe	Pro	Arg	Gly	Gly	Thr	Gly	Ala	Leu	Val
	210					215					220				
Asn	Gly	Met	Ile	Lys	Leu	Phe	Gln	Asp	Leu	Gly	Gly	Glu	Val	Val	Leu
225					230					235					240
Asn	Ala	Arg	Val	Ser	His	Met	Glu	Thr	Val	Gly	Asp	Lys	Ile	Gln	Ala
				245					250					255	
Val	Gln	Leu	Glu	Asp	Gly	Arg	Arg	Phe	Glu	Thr	Cys	Ala	Val	Ala	Ser
			260					265					270		
Asn	Ala	Asp	Val	Val	His	Thr	Tyr	Arg	Asp	Leu	Leu	Ser	Gln	His	Pro
		275					280					285			
Ala	Ala	Ala	Lys	Gln	Ala	Lys	Lys	Leu	Gln	Ser	Lys	Arg	Met	Ser	Asn
	290					295					300				

Ser	Leu	Phe	Val	Leu	Tyr	Phe	Gly	Leu	Asn	His	His	His	Asp	Gln	Leu
305					310					315					320
Ala	His	His	Thr	Val	Cys	Phe	Gly	Pro	Arg	Tyr	Arg	Glu	Leu	Ile	His
				325					330					335	
Glu	Ile	Phe	Asn	His	Asp	Gly	Leu	Ala	Glu	Asp	Phe	Ser	Leu	Tyr	Leu
			340					345					350		
His	Ala	Pro	Cys	Val	Thr	Asp	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Cys	Gly
		355					360					365			
Ser	Tyr	Tyr	Val	Leu	Ala	Pro	Val	Pro	His	Leu	Gly	Thr	Ala	Asn	Leu
	370					375					380				

Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
 385 390 395 400
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
 420 425 430
 Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
 435 440 445
 Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
 450 455 460
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

<210> 9
 <211> 891
 <212> DNA
 <213> Pantoea stewartii

<220>
 <221> CDS
 <222> (1)..(891)

<400> 9
 atg gcg gtt ggc tcg aaa agc ttt gcg act gca tcg acg ctt ttc gac 48
 Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
 1 5 10 15
 gcc aaa acc cgt cgc agc gtg ctg atg ctt tac gca tgg tgc cgc cac 96
 Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
 20 25 30
 tgc gac gac gtc att gac gat caa aca ctg ggc ttt cat gcc gac cag 144
 Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
 35 40 45
 ccc tct tcg cag atg cct gag cag cgc ctg cag cag ctt gaa atg aaa 192
 Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
 50 55 60
 acg cgt cag gcc tac gcc ggt tcg caa atg cac gag ccc gct ttt gcc 240
 Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
 65 70 75 80
 gcg ttt cag gag gtc gcg atg gcg cat gat atc gct ccc gcc tac gcg 288
 Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
 85 90 95
 ttc gac cat ctg gaa ggt ttt gcc atg gat gtg cgc gaa acg cgc tac 336
 Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
 100 105 110

ctg aca ctg gac gat acg ctg cgt tat tgc tat cac gtc gcc ggt gtt	384
Leu Thr Leu 115 Asp Asp Thr Leu Arg 120 Tyr Cys Tyr His Val 125 Ala Gly Val	
gtg ggc ctg atg atg gcg caa att atg ggc gtt cgc gat aac gcc acg	432
Val Gly 130 Leu Met Met Ala Gln 135 Ile Met Gly Val Arg 140 Asp Asn Ala Thr	
ctc gat cgc gcc tgc gat ctc ggg ctg gct ttc cag ttg acc aac att	480
Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe 155 Gln Leu Thr Asn Ile 160	
gcg cgt gat att gtc gac gat gct cag gtg ggc cgc tgt tat ctg cct	528
Ala Arg Asp Ile Val 165 Asp Asp Ala Gln Val 170 Gly Arg Cys Tyr Leu Pro 175	
gaa agc tgg ctg gaa gag gaa gga ctg acg aaa gcg aat tat gct gcg	576
Glu Ser Trp Leu 180 Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr 190 Ala Ala	
cca gaa aac cgg cag gcc tta agc cgt atc gcc ggg cga ctg gta cgg	624
Pro Glu Asn 195 Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg 205 Leu Val Arg	
gaa gcg gaa ccc tat tac gta tca tca atg gcc ggt ctg gca caa tta	672
Glu Ala Glu Pro Tyr Tyr Val 215 Ser Ser Met Ala Gly 220 Leu Ala Gln Leu	
ccc tta cgc tcg gcc tgg gcc atc gcg aca gcg aag cag gtg tac cgt	720
Pro Leu Arg Ser Ala Trp 230 Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg 240	
aaa att ggc gtg aaa gtt gaa cag gcc ggt aag cag gcc tgg gat cat	768
Lys Ile Gly Val Lys 245 Val Glu Gln Ala Gly 250 Lys Gln Ala Trp Asp 255 His	
cgc cag tcc acg tcc acc gcc gaa aaa tta acg ctt ttg ctg acg gca	816
Arg Gln Ser Thr 260 Ser Thr Ala Glu Lys 265 Leu Thr Leu Leu 270 Thr Ala	
tcc ggt cag gca gtt act tcc cgg atg aag acg tat cca ccc cgt cct	864
Ser Gly Gln 275 Ala Val Thr Ser Arg 280 Met Lys Thr Tyr Pro 285 Pro Arg Pro	
gct cat ctc tgg cag cgc ccg atc tag	891
Ala His Leu Trp Gln Arg Pro 295 Ile	

<210> 10
 <211> 296
 <212> PRT
 <213> Pantoea stewartii

<400> 10

Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1 5 10 15

Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
20 25 30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
35 40 45

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys

50

55

60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65 70 75 80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
85 90 95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
100 105 110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
115 120 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
130 135 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145 150 155 160

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
165 170 175

Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
180 185 190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
195 200 205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
210 215 220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225 230 235 240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
245 250 255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
260 265 270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
275 280 285

Ala His Leu Trp Gln Arg Pro Ile
290 295

<210> 11
<211> 528
<212> DNA
<213> Pantoea stewartii

<220>
 <221> CDS
 <222> (1)..(528)

<400> 11
 atg ttg tgg att tgg aat gcc ctg atc gtg ttt gtc acc gtg gtc ggc 48
 Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
 1 5 10 15
 atg gaa gtg gtt gct gca ctg gca cat aaa tac atc atg cac ggc tgg 96
 Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30
 ggt tgg ggc tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gca ttt 144
 Gly Trp Gly Trp His Leu Ser His Glu Pro Arg Lys Gly Ala Phe
 35 40 45
 gaa gtt aac gat ctc tat gcc gtg gta ttc gcc att gtg tcg att gcc 192
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
 50 55 60
 ctg att tac ttc ggc agt aca gga atc tgg ccg ctc cag tgg att ggt 240
 Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80
 gca ggc atg acc gct tat ggt tta ctg tat ttt atg gtc cac gac gga 288
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95
 ctg gta cac cag cgc tgg ccg ttc cgc tac ata ccg cgc aaa ggc tac 336
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110
 ctg aaa cgg tta tac atg gcc cac cgt atg cat cat gct gta agg gga 384
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125
 aaa gag ggc tgc gtg tcc ttt ggt ttt ctg tac gcg cca ccg tta tct 432
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140
 aaa ctt cag gcg acg ctg aga gaa agg cat gcg gct aga tcg ggc gct 480
 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
 145 150 155 160
 gcc aga gat gag cag gac ggg gtg gat acg tct tca tcc ggg aag taa 528
 Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
 165 170 175

<210> 12
 <211> 175
 <212> PRT
 <213> Pantoea stewartii

<400> 12
 Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
 1 5 10 15
 Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
50 55 60

Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145 150 155 160

Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
165 170 175

<210> 13
<211> 61
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(dxs)

<400> 13
tggaagcgct agcggactac atcatccagc gtaataaata acgtcttgag cgattgtgta 60
g 61

<210> 14
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(idi)

<400> 14
tctgatgcgc aagctgaaga aaaatgagca tggagaataa tatgacgtct tgagcgattg 60
tgtag 65

<210> 15
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(lytB)

<400> 15

tttgatattg aagtgctgga aatcgatccg gcactggagg cgtaacgtct tgagcgattg 60
tgtag 65

<210> 16
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(dxr)

<400> 16
gaagcggcgc tggcagacaa agaagcagaa ctgatgcagt tctgacgtct tgagcgattg 60
tgtag 65

<210> 17
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'kan(ygbBP)

<400> 17
gacgcgtcga agcgcgcaca gtctgcgggg caaaacaatc gataacgtct tgagcgattg 60
tgtag 65

<210> 18
<211> 64
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'kan

<400> 18
gaagacgaaa gggcctcgtg atacgcctat ttttataggt tatatgaata tcctccttag 60
ttcc 64

<210> 19
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-T5

<400> 19
ctaaggagga tattcatata acctataaaa ataggcgtat cacgaggccc 50

<210> 20
<211> 70
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(dxs)

<400> 20
ggagtcgacc agtgccaggg tcgggtatct ggcaatatca aaactcatag ttaatttctc 60

ctctttaatg 70

<210> 21
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(idi)

<400> 21
tgggaactcc ctgtgcattc aataaaatga cgtgttccgt ttgcatagtt aatttctcct 60
ctttaatg 68

<210> 22
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(lytB)

<400> 22
ctaccccggc acaaaaacca cgtgggttgg ccaacaggat ctgcatagtt aatttctcct 60
ctttaatg 68

<210> 23
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(dxr)

<400> 23
tgcaaccaat cgagccggtc gagcccagaa tggtagattg cttcatagtt aatttctcct 60
ctttaatg 68

<210> 24
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-T5(ygbBP)

<400> 24
cggccgcccgg aaccacggcg caaacatcca aatgagtggg tgccatagtt aatttctcct 60
ctttaatg 68

<210> 25
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-kanT5(ispA)

<400> 25

aacgaagacg cctctctaac ccctttttaca ccggacaatg agtaacgtct tgagcgattg 60
tgtag 65

<210> 26
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-kanT5(ychB)

<400> 26
ggatcaacgca tcaagttaaa aatggataac tggatagtga aataacgtct tgagcgattg 60
tgtag 65

<210> 27
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-kanT5(gcpE)

<400> 27
gttgcgcgctc tgaccctcaa tgccgaacaa tcaccggcgc agtaacgtct tgagcgattg 60
tgtag 65

<210> 28
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 5'-kanT5(ispB)

<400> 28
accataaacc ctaagttgcc tttgttcaca gtaaggtaat cggggcgctct tgagcgattg 60
tgtag 65

<210> 29
<211> 70
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-kanT5(ispA)

<400> 29
ctgggttgcc tgcttaacgc aggcttcgag ttgctgcgga aagtccatag ttaatttctc 60
ctctttaatg 70

<210> 30
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-kanT5(ychB)

<400> 30
ataaaaaacag attaatgttt gccggagagg gccactgtgt ccgcatagtt aatttctcct 60
ctttaatg 68

<210> 31
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-kanT5(gcpE)

<400> 31
aaatacgtgt tgattttcta cgttgaattg gagcctgggt atgcatagtt aatttctcct 60
ctttaatg 68

<210> 32
<211> 67
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 3'-kanT5(ispB)

<400> 32
cgccatatct tgcgcggtta actcattgat tttttctaaa ttcatagtta atttctcctc 60
tttaatg 67

<210> 33
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer for crt gene cluster

<400> 33
atgacggtct gcgcaaaaaa acacg 25

<210> 34
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer for crt gene cluster

<400> 34
gagaaattat gttgtggatt tggaatgc 28

<210> 35
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Primer T-kan

<400> 35
accgatatc accacttatc tgctc 25

<210> 36
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer B-dxs

 <400> 36
 tggcaacagt cgtagctcct ggggtgg 26

<210> 37
 <211> 32
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer T-T5

 <400> 37
 taacctataa aaataggcgt atcacgaggc cc 32

<210> 38
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer B-idi

 <400> 38
 tcatgctgac ctggtgaagg aatcc 25

<210> 39
 <211> 45
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer B-ispB

 <400> 39
 accataaacc ctaagttgcc ttgtttcaca gtaaggtaat cgggg 45

<210> 40
 <211> 8609
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Plasmid pPCB15

 <400> 40
 cgtatggcaa tgaaagacgg tgagctggtg atatgggata gtgttcaccc ttgttacacc 60
 gttttccatg agcaaactga aacgttttca tcgctctgga gtgaatacca cgacgatttc 120
 cggcagtttc tacacatata ttcgcaagat gtggcgtggt acggtgaaaa cctggcctat 180
 ttccctaaag ggtttattga gaatatgttt ttcgtctcag ccaatccctg ggtgagtttc 240
 accagttttg atttaaactg ggccaatatg gacaacttct tcgcccccggt tttcaccatg 300
 ggcaaataatt atacgcaagg cgacaagggt ctgatgccgc tggcgattca ggttcatcat 360

gccgtctgtg	atggcttcca	tgtcggcaga	atgcttaatg	aattacaaca	gtactgcgat	420
gagtggcagg	gcggggcgta	atTTTTTTaa	ggcagttatt	ggtgcctaga	aatatTTTat	480
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